

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 19, 2004, 01:14:52; Search time 7.02288 Seconds

(without alignments)  
1468.042 Million cell updates/sec

Title: US-10-691-383-2\_COPY\_435\_632

Perfect score: 1039

Sequence: 1 VNFQTSHYERLIGAAELAQR.....GLLGELTTVTTLHQLMTF 198

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	* Query Match Length	ID	Description
1	93.5	90.0	557 1	PRXY_ASCNO
2	85.5	8.2	609 1	PRXC_CURIN
3	85.5	8.2	1819 1	GCPC_HUMAN
4	82.5	7.9	330 1	Y374_METJA
5	82	7.9	567 1	RST2_SCHPO
6	79.5	7.7	158 1	YB06_ECOLI
7	79.5	7.7	419 1	MUA2_STRPY
8	79.5	7.7	419 1	MUA2_STRPY
9	79.5	7.7	922 1	UB23_HUMAN
10	78.5	7.6	206 1	Y236_THBAC
11	77.5	7.5	454 1	SR54_AQUAE
12	77.5	7.5	940 1	PTGA_MYCPN
13	77	7.4	495 1	TOLC_ECOLI
14	76	7.3	394 1	PGK_BACME
15	75.5	7.3	426 1	APBE_MYCLE
16	75.5	7.3	493 1	GALT_LACTC
17	75	7.2	337 1	GLX_XYLET
18	75	7.2	774 1	STP_LAMB
19	74.5	7.2	260 1	OPRI_NEIMC
20	74.5	7.2	835 1	VIRL_AERTU
21	74	7.1	237 1	YE1L_ECOLI
22	74	7.1	611 1	GLMS_PALSO
23	73.5	7.1	154 1	FMN_MORNO
24	73.5	7.1	472 1	GCSE_THREVO
25	73.5	7.1	803 1	DCML_HNDPS
26	73	7.0	603 1	LEPA_STY3
27	73	7.0	1163 1	Y222_HUMAN
28	72.5	7.0	216 1	Y007_TREBP
29	72.5	7.0	304 1	STKG_MOUSE
30	72.5	7.0	316 1	ARCC_BACLI
31	72.5	7.0	398 1	A23D_DROME
32	72.5	7.0	417 1	SAHH_MERTH
33	72.5	7.0	630 1	GIDA_PSEPU

RESULT 1	ID	PRXY_ASCNO	STANDARD	PRT	557 AA
AC	PRXY_ASCNO	STANDARD	PRT	557 AA	
AT	P81701				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Vanadium haloperoxidase (EC 1.11.1.-) (V-BPO).				
OS	Ascopyllum nodosum (Knotted wrack) (Brown seaweed).				
OC	Eukaryota; Stramenopiles; Phaeophyceae; Fucales; Fucaceae;				
OC	Ascopyllum.				
OX	NCBI_TaxID=52969;				
RP	SEQUENCE, X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND FUNCTION.				
RP	MEHLIN=20013071; PubMed=10543953;				
RA	Weyand M., Hecht H.-U., Kiess M., Llaud M.-F., Valtter H.,				
RA	Schomburg D.;				
RT	"X-ray structure determination of a vanadium-dependent				
RT	haloperoxidase from Ascopyllum nodosum at 2.0-A resolution."				
RL	J. Mol. Biol. 293:595-611(1999).				
RN	[2]				
RP	SEQUENCE OF 326-556 FROM N.A., SEQUENCE OF 326-341; 383-426; 471-479				
RP	AND 481-556, AND FUNCTION.				
RX	MEDLINE=96081028; PubMed=8564812;				
RA	Valter H.;				
RL	"Vanadium-dependent haloperoxidases.";				
RL	(In) Sigel H., Sigel A. (eds.);				
RL	Metal ions in biological system-vanadium and its role in life,				
RL	pp.31:325-362, Marcel Dekker, New York (1995).				
CC	-1- CATALYTIC ACTIVITY: Halide + H(2)O(2) + H(+) = HOHal + H(2)O.				
CC	-1- COFACTOR: Vanadium.				
CC	-1- SUBUNIT: Homodimer; disulfide-linked.				
CC	-1- SIMILARITY: TO OTHER BACTERIAL NON-HEME BROMO- AND CHLORO-				
CC	PEROXIDASES.				
DR	PDB: 1OI9; 10-JUN-00.				
DR	InterPro: IPR008934; Acpage VanPerase.				
DR	InterPro: IPR00326; PA_PPase.				
KW	Oxidoreductase; Peroxidase; Vanadium; 3D-structure;				
KW	Pyridoxal.dione carboxylic acid.				
KW	MOD RES				
FT	DISULFID	1	3	3	PYRROLIDONE CARBOXYLIC ACID.
FT	DISULFID	41	41	41	INTERCHAIN (WITH C-41).
FT	DISULFID	77	86	86	INTERCHAIN (WITH C-3).
FT	DISULFID	441	462	462	
FT	DISULFID	544	555	555	
FT	ACT SITE	411	411	411	
FT	ACT SITE	418	418	418	
FT	METAL	486	486	486	
FT	CONFLICT	321	321	321	
FT	CONFLICT	341	341	341	
FT	CONFLICT	403	404	404	
FT	CONFLICT	407	408	408	
FT	CONFLICT	409	409	409	
FT	CONFLICT	441	444	444	
FT	CONFLICT	470	470	470	
FT	HELEX	15	37	37	

08878 pseudomonas  
09924 xylella fas  
09204 listeria in  
09X767 bacillus ha  
P1346 dictyostel  
08287 yersinia pe  
P3281 saccharomyc  
08Y13 bruceella me  
P1773 mycobacteri  
04315 homo sapien  
09290 rickettsia  
P19972 p salt-nedi

T HELIX 50 52  
 T STRAND 53 53  
 T TURN 56 57  
 T STRAND 57 57  
 T TURN 60 60  
 T STRAND 62 63  
 T TURN 66 66  
 T STRAND 68 80  
 T HELIX 83 87  
 T TURN 88 88  
 T HELIX 98 100  
 T STRAND 102 103  
 T TURN 105 108  
 T TURN 118 119  
 T TURN 129 130  
 T HELIX 132 146  
 T TURN 147 149  
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 T TURN 155 157  
 T HELIX 159 170  
 T TURN 172 173  
 T HELIX 174 176  
 T STRAND 178 179  
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 T STRAND 197 197  
 T TURN 200 203  
 T HELIX 210 213  
 T STRAND 216 218  
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 T HELIX 488 512  
 T STRAND 519 522  
 T TURN 524 525

FT STRAND 528 531  
 FT TURN 533 534  
 FT STRAND 537 539  
 FT TURN 540 541  
 FT STRAND 542 543  
 FT TURN 552 554  
 SQ SEQUENCE 557 AA; 60343 MW; E3D8557AB92B16F4 CRC64;  
 Query Match 90.0%; Score 935; DB 1; Length 557;  
 Best Local Similarity 89.4%; Pred. No. 6,9e-81;  
 Matches 177; Conservative 12; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 VNFQSHYFRLIGAMELAGRASCYQKQVHRPAREALGGTLANTIAGDLADPDISILE 60  
 316 VNFQSHYFRLIGAMELAGRASCYQKQVHRPAREALGGTLANTIAGDLADPDISILE 375  
 Db 61 NDELLARVAEINAAQPNNEVTYLLPOAIQVGSPTHPSPSGHATONGAFATYVKALIGL 120  
 376 NAEELKRVAAINAAQPNNEVTYLLPOAIQVGSPTHPSPSGHATONGAFATYVKALIGL 435  
 QY 121 DRGECFPPNPVPSDDGLINFBGACLTGEGEINKAVNVAFGROMLGIHYRFDGIQGL 180  
 436 DRGDCYPPDPVYRDDGLKLIDFRGSCLTFEGEINKAVNVAFGROMLGIHYRFDGIQGL 495  
 Db 181 LGGETTVRTHQELMTF 198  
 496 LGGETTVRTHQELMTF 513  
 QY 496 LGGETTVRTHQELMTF 513  
 Db 496 LGGETTVRTHQELMTF 513  
 RESULT 2  
 ID PRXC\_CURIN STANDARD; PRT: 609 AA.  
 AC P49053;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Vanadium chloroperoxidase (EC 1.11.1.10) (VCPO) (Vanadium chloride peroxidase).  
 GN CPO.  
 OS Curvularia inaequalis.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;  
 OC Pleosporales; Pleosporaceae; Cochliobolus.  
 OX NCBI\_TaxID=38902;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=95262722; PubMed=7744081;  
 RA Simons B.H., Barnett P., Vollbrecht E.G.M., Dekker H.L.,  
 RA Mijsters A.O., Messerschmidt A., Meyer R.;  
 RT "Primary structure and characterization of the vanadium  
 RT chloroperoxidase from the fungus Curvularia inaequalis";  
 RT Eur. J. Biochem. 229:566-574(1995).  
 RL [2]  
 RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
 RP MEDLINE=96133943; PubMed=8552646;  
 RX Messerschmidt A., Meyer R.;  
 RA "X-ray structure of a vanadium-containing enzyme: chloroperoxidase  
 RT from the fungus Curvularia inaequalis";  
 RT Proc. Natl. Acad. Sci. U.S.A. 93:392-396(1996).  
 RL [1]  
 CC -1- CATALYTIC ACTIVITY: 2 RH + 2 chloride + H(2)O(2) = 2 RCl + 2  
 CC H(2)O.  
 CC -1- COFACTOR: Vanadium.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: The N-terminus is blocked.  
 CC -----  
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 DR EMBL: X85369; CAA59686.1; -